Amendments to the Claims/ Listing of Claims

Please amend claims 1, 7, 10 and 18, and cancel claims 12 and 32, as follows. This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Currently amended) A method of identifying a Pin1 WW domain binding agent, said method comprising:

determining the ability of a potential binding agent to compete with a known Pin1 WW domain substrate for binding to a Pin1 WW domain by contacting said potential binding agent with said Pin1 WW domain in the presence of said known Pin1 WW domain substrate,

wherein the potential binding agent is modeled on a computer to fit spatially into a Pin1 WW domain interaction site using a plurality of atomic coordinates obtained from a Pin1 WW domain crystallized in co-complex with a known Pin1 WW domain binding agent, substrate, or inhibitor,

wherein said plurality of atomic coordinates are as set forth in Table 1, and

wherein a potential binding agent which competes with a known Pin1 WW domain substrate for binding to a Pin1 WW domain is identified as a Pin1 WW domain binding agent.

2. (Cancelled)

3. (Previously presented) The method of claim 1, wherein said binding agent is an agonist or antagonist of said Pin1 WW domain.

4. (Original) The method of claim 1, wherein said binding agent is an inhibitory agent.

5. (Original) The method of claim 4, wherein the inhibitory agent is designed from a known inhibitor.

6. (Original) The method of claim 1, wherein said binding agent is a peptide.

7. (Currently amended) ~~The~~ A method ~~of claim 6~~ **of identifying a Pin1 WW domain binding agent, said method comprising:**

determining the ability of a potential binding agent to compete with a known Pin1 WW domain substrate for binding to a Pin1 WW domain by contacting said potential binding agent with said Pin1 WW domain in the presence of said known Pin1 WW domain substrate,

wherein the potential binding agent is modeled on a computer to fit spatially into a Pin1 WW domain interaction site using a plurality of atomic coordinates obtained from a Pin1 WW domain crystallized in co-complex with a known Pin1 WW domain binding agent, and wherein said **known** binding agent has a sequence Tyr-pSer-Pro-Thr-pSer-Pro-Ser (SEQ ID NO:3).

8. (Original) The method of claim 1, wherein said binding agent is selected from the group consisting of a small molecule, a peptidomimetic, and an antibody.

9. (Previously presented) The method of claim 1, further comprising providing a computer with a three-dimensional representation of said interaction site and using a computer algorithm to predict a three-dimensional representation of said potential binding agent.

10. (Currently amended) The method of claim **[[1]]** 7, wherein said plurality of atomic coordinates are as set forth in Table 1.

11. (Original) The method of claim 1, wherein said potential binding agent is designed de novo.

12.-17. (Cancelled)

18. (Currently amended) A computer program on a computer readable medium, said computer program comprising instructions to cause a computer to:

model a potential binding agent that fits spatially into a Pin1 WW domain interaction site using a plurality of atomic coordinates obtained from a Pin1 WW domain crystallized in co-complex with a known Pin1 WW domain binding agent, substrate, or inhibitor, **wherein said plurality of atomic coordinates are as set forth in Table 1**.

19-28. (Cancelled)

29. (Previously presented) A computer program on a computer readable medium, said computer program comprising instructions to cause a computer to:

model a potential binding agent that fits spatially into a Pin1 WW domain interaction site using a plurality of atomic coordinates obtained from a Pin1 WW domain crystallized in co-complex with a known Pin1 WW domain binding agent, wherein said known binding agent has a sequence Tyr-pSer-Pro-Thr-pSer-Pro-Ser (SEQ ID NO:3).

30. (Previously presented) The method of claim 7, further comprising providing a computer with a three-dimensional representation of said interaction site and using a computer algorithm to predict a three-dimensional representation of said potential binding agent.

31. (Previously presented) The method of claim 7, wherein said potential binding agent is designed de novo.

32. (Cancelled)